

Python questions:

To answer some of the questions, you must log in to the student server and start python. Hint: *Use the `help()` function around objects or functions to show documentation or examples of usage.*

Obtaining files:

Once logged on to the student server, and before you start python, use the following command to download the file used in the questions to your home folder. (Enter the command in the server terminal, NOT in the python shell)

```
curl http://www.cbs.dtu.dk/courses/27624/L-HBsAg.clustalw > ~/align.clustalw
```

QUESTIONS:

1. The AlignIO module in BioPython contains functions to read in biological alignments in different formats. Use this module to read in the align.clustalw file that you created in your home directory. The file contains a multiple sequence alignment of proteins. Assign the alignment record to the variable **myalign**. Show the code you used to read the alignment file.
Hint: Import the AlignIO module found inside the Bio module with:

```
from Bio import AlignIO
```

(ignore the error message upon importing the module.)

```
from Bio import AlignIO
myalign = AlignIO.read("align.custalw", "clustal")
```

2. Show the code you would use to display the number of sequences in the alignment.

```
len(myalign)
```

3. Show the code you would use to display the maximum alignment length from the **myalign** alignment object.

```
myalign.get_alignment_length()
```

4. Show the code you would use to save the multiple alignment to the file "align.phy" in phyliip format. *Hint: You will need to use a function inside the AlignIO module.*

```
AlignIO.write(myalign, "align.phy", "phyliip")
```